

SEQUENCE LISTING

<110> Glucksmann, Maria A.

<120> 57658, A NOVEL HUMAN URIDINE KINASE AND
USES THEREOF

<130> 381552001700

<140> 09/896,522

<141> 2001-06-28

<150> 60/216,503

<151> 2000-06-30

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<211> 1624

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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			Met Ala Ser Ala Gly Gly Glu			
			1 5			

gac tgc gag agc ccc gcg ccg gag gcc gac cgt ccg cac cag cgg ccc	162
Asp Cys Glu Ser Pro Ala Pro Glu Ala Asp Arg Pro His Gln Arg Pro	
10 15 20	

ttc ctg ata ggg gtg agc ggc ggc act gcc agc ggg aag tcg acc gtg	210
Phe Leu Ile Gly Val Ser Gly Gly Thr Ala Ser Gly Lys Ser Thr Val	
25 30 35	

tgt gag aag atc atg gag ttg ctg gga cag aac gag gtg gaa cag cgg	258
Cys Glu Lys Ile Met Glu Leu Leu Gly Gln Asn Glu Val Glu Gln Arg	
40 45 50 55	

cag cgg aag gtg gtc atc ctg agc cag gac agg ttc tac aag gtc ctg	306
Gln Arg Lys Val Val Ile Leu Ser Gln Asp Arg Phe Tyr Lys Val Leu	
60 65 70	

acg gca gag cag aag gcc aag gcc ttg aaa gga cag tac aat ttt gac	354
Thr Ala Glu Gln Lys Ala Lys Ala Leu Lys Gly Gln Tyr Asn Phe Asp	
75 80 85	

cat cca gat gcc ttt gat aat gat ttg atg cac agg act ctg aag aac	402
His Pro Asp Ala Phe Asp Asn Asp Leu Met His Arg Thr Leu Lys Asn	
90 95 100	

atc gtg gag ggc aaa acg gtg gag gtg ccg acc tat gat ttt gtg aca Ile Val Glu Gly Lys Thr Val Glu Val Pro Thr Tyr Asp Phe Val Thr 105 110 115	450
cac tca agg tta cca gag acc acg gtg gtc tac cct gcg gac gtg gtt His Ser Arg Leu Pro Glu Thr Thr Val Val Tyr Pro Ala Asp Val Val 120 125 130 135	498
ctg ttt gag ggc atc ttg gtg ttc tac agc cag gag atc cgg gac atg Leu Phe Glu Gly Ile Leu Val Phe Tyr Ser Gln Glu Ile Arg Asp Met 140 145 150	546
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ctg acg cag tac acc acc ttc gtg aag ccg gcc ttc gag gag ttc tgc Leu Thr Gln Tyr Thr Thr Phe Val Lys Pro Ala Phe Glu Glu Phe Cys 185 190 195	690
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aat ggt gac atc tgc aaa tgg cac cga gga ggg tcc aat ggg cgg agc Asn Gly Asp Ile Cys Lys Trp His Arg Gly Gly Ser Asn Gly Arg Ser 235 240 245	834
tac aag cgg acc ttt tct gag cca ggg gac cac cct ggg atg ctg acc Tyr Lys Arg Thr Phe Ser Glu Pro Gly Asp His Pro Gly Met Leu Thr 250 255 260	882
tct ggc aaa cgg tca cat ttg gag tcc agc agc aga ccc cac tga Ser Gly Lys Arg Ser His Leu Glu Ser Ser Ser Arg Pro His * 265 270 275	927
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aacctgatcg	tcagcacat	ccaggacatt	ctgaatgggt	acatctgcaa	atggcaccga	720
ggaggggtcca	atgggcggag	ctacaagcgg	accttttctg	agccagggga	ccaccctggg	780
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<212> PRT

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<223> Consensus amino acid sequence

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		20					25					30			
Ile	Glu	Gly	Asn	Pro	Asp	Ser	Asn	Thr	Gly	Asp	Ser	Phe	Leu	Arg	Leu
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Asp	Arg	Phe	Tyr	Met	Asp	Leu	His	Leu	Glu	Asp	Arg	Lys	Arg	Ala	Gly
	50				55					60					
Asn	Lys	His	Tyr	Ser	Phe	Phe	Ser	Pro	Glu	Ala	Asn	Asp	Phe	Asp	Leu
65				70					75				80		
Leu	Tyr	Glu	Val	Phe	Lys	Glu	Leu	Lys	Glu	Gly	Lys	Ser	Val	Asp	Lys
			85					90					95		
Pro	Ile	Tyr	Asn	His	Val	Thr	Gly	Glu	Arg	Asp	Pro	Asp	Gly	Gln	Glu
		100					105						110		
Pro	Gly	Thr	Phe	Thr	Asp	Trp	Pro	Glu	Leu	Ile	Glu	Gly	Ala	Asp	Val
	115				120						125				
Leu	Val	Ile	Glu	Gly	Leu	His	Ala	Leu	Tyr	Asp	Glu	Arg	Glu	Val	Asn
	130				135					140					
Val	Ala	Gln	Leu	Leu	Asp	Leu	Lys	Ile	Tyr	Val	Asp	Pro	Asp	Ile	Asp
145				150					155					160	
Leu	Glu	Leu	Ala	Arg	Lys	Ile	Gln	Arg	Asp	Met	Ala	Glu	Arg	Gly	His
			165				170						175		
Ser	Leu	Glu	Gly	Val	Leu	Asp	Ser	Ile	Glu	Lys	Arg	Arg	Lys	Pro	Asp
	180					185						190			
Tyr	Val	Asn	Tyr	Ile	Ala	Pro	Gln	Phe	Ser	Tyr	Ala	Asp	Leu	Ile	Ile
	195					200						205			
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			20					25					30		
Glu	Gln	Tyr	Met	Lys	Phe	Val	Lys	Pro	Met	Tyr	Glu	Gln	Phe	Ile	Glu
		35					40					45			
Pro	Thr	Lys	Lys	Tyr	Ala	Asp	Ile	Ile	Ile	Pro	Arg	Gly	Gly	Asp	Asn
	50					55					60				
His	Val	Ala	Ile	Asp	Leu	Ile	Val	Gln	His	Ile	Gln	Ser	Ile	Leu	Asn
65					70					75				80	
Glu	Gly	Leu	Ser	Ser	Gln	His	Thr	Asn	Tyr	Met	Val	Asn	Arg	Ser	Tyr
			85						90					95	
Lys	Arg	Thr	Phe	Ser	Glu	Pro	Gly	Asp	His	Pro	Gly	Tyr	Thr	Pro	Ser
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			20					25					30		
Ile	Ile	Ser	Gln	Asp	Asn	Tyr	Tyr	Lys	Asp	Leu	Ser	Glu	Leu	Asp	Met
		35				40					45				
Glu	Glu	Arg	Lys	Glu	Asn	Asn	Tyr	Asn	Phe	Asp	His	Pro	Asp	Ala	Phe
	50				55					60					
Asp	Phe	Asp	Leu	Leu	Tyr	Glu	His	Leu	Lys	Asx	Leu	Lys	Asn	Gly	Lys
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Ser	Val	Glu	Val	Pro	Ile	Tyr	Asp	Phe	Lys	Thr	His	His	Arg	Arg	Lys
			85					90					95		
Asp	Glu	Thr	Val	Thr	Ile	Glu	Pro	Ala	Asp	Val	Ile	Ile	Leu	Glu	Gly
			100					105					110		
Ile	Tyr	Ala	Leu	Tyr	Asp	Glu	Arg	Ile	Arg	Asp	Leu				
		115					120								